

## SEQUENCE LISTING

<110> GlaxoSmithKline Biologicals s.a.

<120> Novel Compounds

<130> B45282

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 909

<212> DNA

<213> Dermatophagoides pteronyssinus

<220>

<221> CDS

<222> (1)...(906)

<400> 1

cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48  
Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn  
1 5 10 15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96  
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe  
20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144  
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His

35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192  
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50 55 60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240  
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu

65 70 75 80

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288  
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu

85 90 95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336  
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly

100 105 110

tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc 384  
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu

115 120 125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432  
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp

130 135 140

tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480  
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile

145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528  
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

165 170 175

gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc 576  
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly  
180 185 190

att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg 624  
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg  
195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672  
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile  
210 215 220

aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720  
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln  
225 230 235 240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768  
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly  
245 250 255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816  
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp  
260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864  
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile  
275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906  
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu  
290 295 300

taa 909

&lt;210&gt; 2

&lt;211&gt; 302

&lt;212&gt; PRT

&lt;213&gt; Dermatophagoides pteronyssinus

&lt;400&gt; 2

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn

1 5 10 15

Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

20 25 30

Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His

35 40 45

Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50 55 60

Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu

65 70 75 80

Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu

85 90 95

Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly

100 105 110

Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu

115 120 125

Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp

130 135 140

Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile

145 150 155 160

Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

165 170 175

Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly

180 185 190

Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg

195 200 205

Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile

210 215 220

Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln  
 225            230            235            240  
 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly  
              245            250            255  
 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp  
              260            265            270  
 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile  
              275            280            285  
 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu  
              290            295            300

<210> 3

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> C4R mutant of ProDer p 1

<400> 3

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn  
 1            5            10            15  
 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe  
              20            25            30  
 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His  
              35            40            45  
 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser  
              50            55            60  
 Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu  
 65            70            75            80  
 Thr Asn Ala Arg Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu  
              85            90            95  
 Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly

100                      105                      110  
 Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu  
 115                      120                      125  
 Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp  
 130                      135                      140  
 Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile  
 145                      150                      155                      160  
 Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr  
 165                      170                      175  
 Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly  
 180                      185                      190  
 Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg  
 195                      200                      205  
 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile  
 210                      215                      220  
 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln  
 225                      230                      235                      240  
 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly  
 245                      250                      255  
 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp  
 260                      265                      270  
 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile  
 275                      280                      285  
 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu  
 290                      295                      300

&lt;210&gt; 4

&lt;211&gt; 909

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(906)

&lt;223&gt; C4R mutant of ProDer p 1

&lt;400&gt; 4

cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48  
Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn  
1 5 10 15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96  
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe  
20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144  
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His  
35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192  
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser  
50 55 60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240  
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu  
65 70 75 80

acc aac gcc cgt agt atc aac ggc aat gcc ccc gct gag att gat ctg 288  
Thr Asn Ala Arg Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu  
85 90 95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336  
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly  
100 105 110

tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc 384

Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu

115 120 125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432

Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp

130 135 140

tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480

Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile

145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528

Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

165 170 175

gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc 576

Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly

180 185 190

att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg 624

Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg

195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672

Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile

210 215 220

aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720

Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln

225 230 235 240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768

Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly

245 250 255



tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816  
 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp  
 260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864  
 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile  
 275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906  
 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu  
 290 295 300

taa 909

<210> 5

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> C31R mutant of ProDer p 1

<400> 5

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn  
 1 5 10 15  
 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe  
 20 25 30  
 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His  
 35 40 45  
 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser  
 50 55 60  
 Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu  
 65 70 75 80

Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu  
85 90 95  
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Arg Gly  
100 105 110  
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu  
115 120 125  
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp  
130 135 140  
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile  
145 150 155 160  
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr  
165 170 175  
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly  
180 185 190  
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg  
195 200 205  
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile  
210 215 220  
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln  
225 230 235 240  
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly  
245 250 255  
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp  
260 265 270  
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile  
275 280 285  
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu  
290 295 300

&lt;210&gt; 6

&lt;211&gt; 909

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(906)

&lt;223&gt; C31R mutant of ProDer p 1

&lt;400&gt; 6

cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn

1 5 10 15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96

Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144

Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His

35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192

Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50 55 60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240

Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu

65 70 75 80

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288

Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu

85 90 95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc cgt ggg 336

Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Arg Gly

100	105	110	
tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc 384			
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu			
115	120	125	
gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432			
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp			
130	135	140	
tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480			
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile			
145	150	155	160
gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528			
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr			
165	170	175	
gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc 576			
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly			
180	185	190	
att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg 624			
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg			
195	200	205	
gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672			
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile			
210	215	220	
aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720			
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln			
225	230	235	240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768  
 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly  
 245 250 255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816  
 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp  
 260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864  
 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile  
 275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906  
 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu  
 290 295 300

taa 909

<210> 7

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> C65R mutant of ProDer p 1

<400> 7

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn  
 1 5 10 15  
 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe  
 20 25 30  
 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His  
 35 40 45  
 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50            55            60  
 Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu  
 65            70            75            80  
 Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu  
              85            90            95  
 Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly  
              100            105            110  
 Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu  
              115            120            125  
 Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp  
              130            135            140  
 Arg Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile  
 145            150            155            160  
 Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr  
              165            170            175  
 Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly  
              180            185            190  
 Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg  
              195            200            205  
 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile  
              210            215            220  
 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln  
 225            230            235            240  
 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly  
              245            250            255  
 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp  
              260            265            270  
 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile  
              275            280            285  
 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu  
              290            295            300

&lt;210&gt; 8

<211> 909

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(906)

<223> C65R mutant of ProDer p 1

<400> 8

cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn

1 5 10 15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96

Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144

Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His

35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192

Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50 55 60

gcc gag gct ttc gaa cac ctt aag acc cag ttg gat ctc aac gcg gag 240

Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu

65 70 75 80

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288

Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu

85 90 95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336  
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly  
100 105 110

tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc 384  
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu  
115 120 125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432  
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp  
130 135 140

cgt gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480  
Arg Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile  
145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528  
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr  
165 170 175

gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc 576  
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly  
180 185 190

att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg 624  
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg  
195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672  
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile  
210 215 220

aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720



Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln  
 225            230            235            240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768  
 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly  
                  245            250            255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816  
 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp  
                  260            265            270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864  
 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile  
                  275            280            285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906  
 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu  
                  290            295            300

taa 909

<210> 9

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> C71R mutant of ProDer p 1

<400> 9

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn  
 1            5            10            15  
 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe  
                  20            25            30

Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His  
 35 40 45  
 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser  
 50 55 60  
 Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu  
 65 70 75 80  
 Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu  
 85 90 95  
 Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly  
 100 105 110  
 Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu  
 115 120 125  
 Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp  
 130 135 140  
 Cys Ala Ser Gln His Gly Arg His Gly Asp Thr Ile Pro Arg Gly Ile  
 145 150 155 160  
 Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr  
 165 170 175  
 Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly  
 180 185 190  
 Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg  
 195 200 205  
 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile  
 210 215 220  
 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln  
 225 230 235 240  
 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly  
 245 250 255  
 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp  
 260 265 270  
 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile  
 275 280 285  
 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu  
 290 295 300

<210> 10

<211> 909

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(906)

<223> C71R mutant of ProDer p 1

<400> 10

cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48  
Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn  
1 5 10 15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96  
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe  
20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144  
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His  
35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192  
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser  
50 55 60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240  
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu  
65 70 75 80

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288  
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu  
85 90 95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336  
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly  
100 105 110

tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc 384  
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu  
115 120 125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432  
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp  
130 135 140

tgc gcc tcc caa cac gga cgt cat ggg gat acg att ccc aga ggt atc 480  
Cys Ala Ser Gln His Gly Arg His Gly Asp Thr Ile Pro Arg Gly Ile  
145 150 155 160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528  
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr  
165 170 175

gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc 576  
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly  
180 185 190

att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg 624  
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg  
195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672  
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile

210                    215                    220

aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720  
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln  
225                    230                    235                    240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768  
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly  
245                    250                    255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816  
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp  
260                    265                    270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864  
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile  
275                    280                    285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906  
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu  
290                    295                    300

taa 909

&lt;210&gt; 11

&lt;211&gt; 302

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; C103R mutant of ProDer p 1

&lt;400&gt; 11

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn

1            5            10            15  
 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe  
           20            25            30  
 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His  
           35            40            45  
 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser  
           50            55            60  
 Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu  
 65            70            75            80  
 Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu  
           85            90            95  
 Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly  
           100            105            110  
 Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu  
           115            120            125  
 Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp  
           130            135            140  
 Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile  
 145            150            155            160  
 Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr  
           165            170            175  
 Val Ala Arg Glu Gln Ser Arg Arg Arg Pro Asn Ala Gln Arg Phe Gly  
           180            185            190  
 Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg  
           195            200            205  
 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile  
           210            215            220  
 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln  
 225            230            235            240  
 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly  
           245            250            255  
 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp  
           260            265            270  
 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile

275                      280                      285  
 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu  
 290                      295                      300

<210> 12

<211> 909

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(906)

<223> C103R mutant of ProDer p 1

<400> 12

cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48  
 Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn  
 1                      5                      10                      15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96  
 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe  
 20                      25                      30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144  
 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His  
 35                      40                      45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192  
 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser  
 50                      55                      60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240

Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu  
 65                      70                      75                      80

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288  
 Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu  
                     85                      90                      95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336  
 Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly  
                     100                      105                      110

tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc 384  
 Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu  
                     115                      120                      125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432  
 Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp  
                     130                      135                      140

tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480  
 Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile  
 145                      150                      155                      160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528  
 Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr  
                     165                      170                      175

gta gct agg gag cag tcc cgt cgc cgt cct aac gca cag cgc ttc ggc 576  
 Val Ala Arg Glu Gln Ser Arg Arg Arg Pro Asn Ala Gln Arg Phe Gly  
                     180                      185                      190

att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg 624  
 Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg  
                     195                      200                      205



gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672  
 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile  
 210 215 220

aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720  
 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln  
 225 230 235 240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768  
 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly  
 245 250 255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816  
 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp  
 260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864  
 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile  
 275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906  
 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu  
 290 295 300

taa 909

<210> 13

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> C117R mutant of ProDer p 1

&lt;400&gt; 13

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn

1            5            10            15

Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

20            25            30

Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His

35            40            45

Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50            55            60

Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu

65            70            75            80

Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu

85            90            95

Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly

100            105            110

Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu

115            120            125

Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp

130            135            140

Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile

145            150            155            160

Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

165            170            175

Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly

180            185            190

Ile Ser Asn Tyr Arg Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg

195            200            205

Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile

210            215            220

Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln

225            230            235            240

Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly

245            250            255

Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp

260 265 270

Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile

275 280 285

Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu

290 295 300

<210> 14

<211> 909

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(906)

<223> C117R mutant of ProDer p 1

<400> 14

cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn

1 5 10 15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96

Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144

Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His

35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192

Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50                      55                      60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240  
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu  
65                      70                      75                      80

acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg 288  
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu  
85                      90                      95

cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg 336  
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly  
100                      105                      110

tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc 384  
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu  
115                      120                      125

gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac 432  
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp  
130                      135                      140

tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc 480  
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile  
145                      150                      155                      160

gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac 528  
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr  
165                      170                      175

gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc 576  
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly  
180                      185                      190

att tcc aat tat cgt cag atc tac ccc cct aat gcc aac aag atc agg 624  
 Ile Ser Asn Tyr Arg Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg  
 195 200 205

gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc 672  
 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile  
 210 215 220

aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag 720  
 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln  
 225 230 235 240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768  
 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly  
 245 250 255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816  
 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp  
 260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864  
 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile  
 275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906  
 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu  
 290 295 300

taa 909

<210> 15

<211> 108

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 15

ttaagaccca gtttgatctc aacgcggaga ccaacgcccg tatcaacggc aatgcccccg 60  
ctgagattga tctgcgccag atgaggaccg tgactcccat ccgcatgc 108

<210> 16

<211> 103

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 16

cggatgggag tcacggtcct catctggcgc agatcaatct cagcgggggc attgccgttg 60  
atactacggg cgttggtctc cgcgttgaga tcgaaactgg gtc 103

<210> 17

<211> 92

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 17

caaggcggcc gtgggtcttg ttgggccttt tcaggcgtgg ccgcgacaga gtcggcatac 60  
ctcgcgtatc ggaatcagag cctggacctc gc 92

<210> 18

<211> 99

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 18

tcagcgagggt ccaggctctg attccgatac gcgagggtatg ccgactctgt cgcggccacg 60

cctgaaaagg cccaacaaga cccacggccg ccttgcatg 99

<210> 19

<211> 83

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 19

tgagcaggag ctcggtgacc gtgcctccca acacggatgt catggggata cgattcccag 60

aggtatcgaa tacatccagc ata 83

<210> 20

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 20

ctggatgtat tcgatactc tgggaatcgt atcccccattg acatccgtgt tgggaggcac 60

ggtcaacgcg ctctgc 77

<210> 21

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 21

actgacaggc ctcggccgag ctccattaa 29

<210> 22

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 22

cagtcaccta ggtctagact cgaggggat 29

<210> 23

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 23

ggctttcgaa caccttaaga cccag 25

<210> 24



<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 24

gctccctagc tacgtatcgg taatagc

27

<210> 25

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 25

cctcgcgtat cggcaacaga gcctggacc

29

<210> 26

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 26

ggtccaggct ctgtgccga tacgcgagg

29